

## Primitive Accession Derived Germplasm by Cultivar Crosses as Sources for Cotton Improvement: II. Genetic Effects and Genotypic Values

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### ABSTRACT

Primitive accession derived germplasm of cotton, *Gossypium hirsutum* L., may provide useful traits for cultivar improvement. The ability to predict advanced generation performance when crossed with commercial cultivars would enhance their utility and encourage their use in breeding programs. Our objective for this study was to predict genetic effects for day-neutral derived lines derived from primitive accessions and crossed to cultivars using a mixed linear model approach. Parents and  $F_2$  populations were grown at two field locations in 1998 and 1999 and parents and  $F_3$  were grown at two locations in 2000. Lint yield, yield components, and fiber quality traits were evaluated. An additive-dominance additive  $\times$  additive (ADAA) model was used for genetic analysis. A mixed linear model, minimum norm quadratic unbiased estimation (MINQUE) was used to predict genetic effects and genotype values. Generally, the female cultivar parents had higher additive effects for lint yield and lint percentage; however, these females generally had lower additive effects for fiber strength. Significant AA effects widely existed among parents and  $F_2$  populations for lint percentage, boll weight, and fiber strength. The correlation coefficients between observed values and predicted values were mainly high among traits and environments. These data suggest that it is appropriate to use the ADAA genetic model to predict genetic effects and hybrid genotypic values for advanced generations. Our study showed that fiber strength may be significantly improved over that of the female parents, while the lint yield was slightly but not significantly predicted to be less than their female parents. This study suggested that day-neutral primitive germplasm accessions provided a valuable gene resource for selecting high yielding lines with significantly improved fiber strength.

IMPROVING COTTON FIBER QUALITY and lint yield remains challenging for cotton breeders. Many of the current high-yielding, commercial upland cultivars do not possess the fiber quality desired by the textile industry. In developing new cultivars, it is important to utilize variability from diverse plant genetic resources. This can limit vulnerability to pests and diseases, while providing useful variation that can be used to form new favorable genetic combinations. However, Van Esbroeck and Bowman (1998) observed that parental genetic diversity, as estimated by coefficient of parentage, was not imperative for cotton improvement. To improve breeding efficiency when using diverse germplasm in developing high-yielding and acceptable fiber-quality cultivars, it is important to understand the genetic effects of these traits.

Primitive accessions of cotton have been reported to have useful genetic variability (Percival, 1987; McCarty

et al., 1995, 1998a, 1998b). Their use has been limited because most require short days to initiate flowers and produce fruit. This requires crosses to be made in a greenhouse or in a tropical nursery. A backcross breeding program has been in place for a number of years to incorporate day-neutral genes into the primitive accessions so they will flower and can be crossed in most cotton breeding nurseries (McCarty et al., 1979; McCarty and Jenkins, 1993). Day-neutral  $F_5$ ,  $BC_1F_5$ ,  $BC_2F_5$ ,  $BC_3F_5$ , and  $BC_4F_5$  progenies were evaluated for several agronomic and fiber traits and useful genetic variability for these traits were reported by McCarty et al. (1995, 1998a, 1998b).

One of the ways to improve fiber quality and cotton yield is to transfer genes into high yielding cultivars from primitive accession germplasm which possess variability for these traits. In this research, crosses were made between five high yielding cultivars and 14 day-neutral derived germplasm lines at Mississippi State, MS (McCarty et al., 2000, 2003). The objective of this study was to predict genetic effects and genotypic values in different generations for agronomic and fiber traits. This research provides insight into how to better utilize these accessions in breeding programs.

### MATERIALS AND METHODS

#### Plant Material and Experimental Design

Day-neutral lines have been developed from photoperiodic primitive accessions. Lines have been selected that have good fiber strength and contain variability for other traits. Fourteen primitive, accession-derived lines were crossed to five cultivars in 1997. Parents and their  $F_2$  or  $F_3$  populations were grown in field plots in 1998 through 2000 and evaluated for yield and fiber quality (McCarty et al., 2000, 2003).

An additive-dominance additive  $\times$  additive (ADAA) and  $G \times E$  interaction genetic model was employed for data analysis (Zhu, 1994). A mixed model, minimum norm quadratic unbiased estimation (MINQUE) approach was used to estimate genetic variance components. The genetic effects and genotype values were predicted by the Adjusted Unbiased Prediction (AUP) method (Zhu, 1993; Zhu and Weir, 1996). The prediction equations for parents and hybrids are listed as follows:

At a specific environment for a parent:

$$\mu + 2A_i + D_{ii} + 4AA_{ii} + 2AE_{hi} + DE_{hii} + 4AAE_{hii}$$

Over environments for a parent:

$$\mu + 2A_i + D_{ii} + 4AA_{ii}$$

At a specific environment for predicted hybrid at generation  $n$  ( $F_n$ ):

**Abbreviations:** AA, additive  $\times$  additive effect; AD, additive dominance model; ADAA, additive-dominance, additive  $\times$  additive model; MINQUE, minimum norm quadratic unbiased estimation.

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$$\mu + (A_i + A_j) + (1/2)^{n-1} D_{ij} + [(2^{n-1} - 1)/2^n] \\ (D_{ii} + D_{jj}) + (AA_{ii} + AA_{jj} + 2AA_{ij}) + (AE_{hi} + \\ AE_{hj}) + (1/2)^{n-1} DE_{hij} + [(2^{n-1} - 1)/2^n] \\ (DE_{hii} + DE_{hjj}) + (AAE_{hii} + AAE_{hjj} + 2AAE_{hij})$$

Over environments for predicted hybrid at generation  $n$  ( $F_n$ ):

$$\mu + (A_i + A_j) + (1/2)^{n-1} D_{ij} + [(2^{n-1} - 1)/2^n] \\ (D_{ii} + D_{jj}) + (AA_{ii} + AA_{jj} + 2AA_{ij})$$

All effects are defined in McCarty et al. (2004).

Jackknifing over blocks within environments was used to estimate standard errors and the predicted effects (Miller, 1974). The degrees of freedom were 19 and  $t$  tests were used for testing significance of each parameter studied. The data set was analyzed by a program written in C++.

## RESULTS AND DISCUSSION

### Genetic Effects

On the basis of the ADAA genetic model, additive, dominance, additive  $\times$  additive epistasis, and genotype  $\times$  environment ( $G \times E$ ) genetic effects were predicted by the AUP method for agronomic traits, micronaire reading, elongation, and fiber strength. Since cotton breeders are more interested in additive and additive  $\times$  additive epistasis effects, which are important for pure line improvement, only these genetic effects will be addressed in this study. The predicted additive effects for agronomic and fiber traits are summarized in Table 1 and additive  $\times$  additive epistasis effects are summarized in Table 2.

Generally, the female commercial cultivar parents, P1-P5 had higher lint yield, and lint percentage than the primitive derived male parents, P6-P19; however, these female parents generally had fewer positive additive effects for fiber strength (Table 1). Results indicate that P1, P2, P3, and P5 can be used as parents for improving lint yield, while the use of P8, P9, P11, P12, P13, P17, P18, and P19 as parents will decrease lint yield. These results indicate that to improve yield, commercial

cultivars are still better sources for the short term; however, for improving yield components that may lead to future yield improvements, primitive derived germplasm can be a valuable source. For example an additive effect for lint percentage was significantly detected for all parents except P9. In addition to the five commercial cultivars, P18 and P19 can be used for lint percentage improvement. Thirteen out of 19 parents had significant additive effects for boll weight. P1, P4, P10, P11, P12, P13, and P19 can be used for developing larger boll lines, while P6, P9, P17, and P18 can be used to develop smaller boll lines. For improving fiber strength, parents 8, 9, 11, 12, 14, 15, 16, and 17 are good choices. For improving 2.5% span length, parents 1, 4, 5, 14, 17, and 19 are good choices. For improving fiber elongation, parents 1, 2, 5, 6, and 18 are good choices.

Just as additive effects are transferable to the offspring progenies, so are additive  $\times$  additive epistasis effects. Thus, additive  $\times$  additive epistasis effects are also important for selection of pure lines in a breeding program. All agronomic traits and fiber traits, except fiber span length, expressed additive  $\times$  additive epistasis effects. One parent (P15) expressed significant negative AA effects for several different traits, while 12 crosses expressed significant AA effects for the same trait. Significant AA effects widely exist among parents and  $F_2$  populations for lint percentage, boll weight, and fiber strength (Table 2). For example, 19 parents and 31 crosses expressed significant AA effects for lint percentage; 12 parents and 32 crosses expressed significant AA effects for boll weight; 15 parents and 22 crosses expressed significant AA effects for fiber strength. Not all significant effects were desirable because some move the trait in an undesirable direction.

If the AA interaction effect between two parents is greater than the mean AA interaction effect within two parents [ $AA_{ij} - (AA_{ii} + AA_{jj})/2 > 0$ ], the genotypic value for the hybrid between the two parents in later generations will be potentially greater than the mid-parent genotypic values. Our results showed that  $AA_{ij}$  is numer-

**Table 1. Predicted additive effects for lint yield (LYLD, kg ha<sup>-1</sup>), lint percent, boll weight (BW, g), micronaire reading (Mic), elongation (E1, %), strength (T1, kNm kg<sup>-1</sup>), 50% span length (SL50, mm) and 2.5% span length (SL2.5, mm).**

Parent	LYLD	Lint %	BW	Mic	E1	T1	SL50†	SL2.5†
1. DPL50	71**	0.79**	0.09**	-0.06*	0.29**	-16.41**	0.08	0.47**
2. DES119	111**	2.29**	0.05	0.07*	0.35**	-3.00*	0.11*	0.27**
3. ST474	72**	2.00**	0.04	0.18**	-0.01	-5.68**	0.04	0.24**
4. DPL90	26	1.13**	0.18**	0.02	-0.28**	3.40	0.03	0.45**
5. SG125	105**	1.60**	0.05	-0.01	0.49**	-14.97**	0.26**	0.45**
6. M75-1	18	-0.42**	-0.22**	0.12**	0.23**	1.98	-0.21**	-1.19**
7. M1388-1	-12	-0.37**	-0.06*	0.05*	-0.03	0.98	-0.15**	-0.68**
8. M1388-2	-44**	-0.66**	-0.08*	-0.06	-0.34**	5.18**	0.07	0.11
9. M1388-3	-44**	-0.15	-0.51**	0.08**	0.11	4.98**	-0.22**	-0.48**
10. M239-1	-19	-0.54**	0.21**	0.12**	0.02	0.22	-0.03	-0.25**
11. M239-2	-40**	-1.17**	0.07*	0.25**	-0.32**	4.66**	0.04	-0.21**
12. M239-3	-48**	-0.99**	0.06**	0.04**	0.03	4.78**	-0.08	-0.22**
13. M239-4	-46**	-1.56**	0.35**	-0.14**	0.12	-0.36	-0.01	0.09
14. M239-5	-8	-0.83**	-0.03	-0.07*	-0.02	2.95**	0.02	0.19**
15. M239-6	-8	-0.38**	0.06	0.02	-0.32**	4.03**	0.01	-0.06
16. M239-7	-3	-1.22**	0.04	0.26**	-0.44**	6.07**	-0.10**	-0.48**
17. M237-1	-39**	-0.86**	-0.21**	-0.39**	-0.16*	8.76**	0.13**	0.64**
18. M237-2	-42**	0.58**	-0.16**	-0.15**	0.39**	-2.81*	-0.05	0.12
19. M237-3	-47*	0.92**	0.10**	-0.23**	0.03	-0.30	0.11*	0.62**

\* Significant at  $P \leq 0.05$ .

\*\* Significant at  $P \leq 0.01$ .

† AD model was used for 50% span length (SL50) and 2.5% span length (SL2.5).

**Table 2. Predicted A\*A epistasis effects for lint yield (LYLD, kg ha<sup>-1</sup>), lint percent, boll weight (BW, g), micronaire (Mic), elongation (E1, %), and strength (T1, kNm kg<sup>-1</sup>)†.**

Cross‡	LYLD	Lint%	BW	Mic	E1	T1
1×1	8	0.44***	0.02	0.02**	0.21***	-3.80***
2×2	-28	0.85***	-0.09**	-0.03**	0.16***	-3.60***
3×3	-3	1.47***	-0.02	-0.02	0.05	-4.36***
4×4	6	0.85***	-0.05**	-0.01	-0.04	-2.41***
5×5	-15	1.08***	-0.02	0.02	0.15***	-2.06***
6×6	-51*	-0.97***	-0.07**	0.00	0.16***	0.62
7×7	-21	-0.24***	-0.02	0.02*	-0.14**	1.26*
8×8	-39	-0.54***	-0.08***	-0.03	0.05	4.77**
9×9	-52*	-0.45***	-0.07***	-0.10	-0.03	5.39***
10×10	-50*	-0.39***	-0.03*	-0.01	-0.15***	2.09***
11×11	-54*	-0.70***	-0.05***	-0.02	0.04*	0.79
12×12	-40*	-0.62***	-0.03*	0.04**	-0.01	2.74***
13×13	-37*	-0.37***	-0.04	-0.03**	-0.06	2.41**
14×14	-39*	-0.28***	-0.04*	-0.00	-0.02	0.50
15×15	-27**	-0.22***	-0.06**	0.03**	-0.05	2.25**
16×16	-50*	-0.71***	-0.02	0.03**	-0.15***	4.84***
17×17	-37	-0.52***	0.01	-0.00	-0.09**	1.58
18×18	-21	-0.42***	-0.08**	-0.06***	-0.17***	3.00***
19×19	-43	-0.28***	-0.06**	-0.08***	-0.07*	2.34**
1×6	24	0.74**	-0.08**	-0.00	-0.01	0.14
1×7	-6	-0.07	-0.05*	0.01	-0.02	-2.17**
1×8	5	-0.09	0.01	-0.02	-0.15***	-0.80
1×9	-7	0.20*	-0.07*	0.04	0.03	-2.28**
1×10	3	-0.04	0.12***	0.01	0.05	-0.88
1×11	-2	-0.13	0.02	0.06	-0.03	-0.06
1×12	-2	0.15	0.01	-0.02	0.11	-0.90
1×13	-13	-0.43***	0.06	-0.05**	0.23***	-3.33***
1×14	17*	-0.26***	-0.01	0.00	-0.02	0.94
1×15	28**	-0.12	0.07**	0.02	-0.15**	0.99
1×16	-2	-0.12	-0.01	0.02	-0.12**	-0.60
1×17	4	-0.24*	-0.02	-0.10***	-0.11**	0.84
1×18	16	0.39***	-0.04**	-0.09***	0.30***	-2.55**
1×19	23**	0.30**	0.05**	-0.01	-0.06	-3.29***
2×6	29*	0.21**	-0.00	0.07***	0.08	-0.55
2×7	14	0.09	-0.04*	0.03	0.14*	0.30
2×8	15	0.09	0.05*	-0.01	-0.15	0.68
2×9	11	-0.04	-0.08***	0.02	0.16**	1.42
2×10	27	-0.21***	0.07**	0.04*	0.10*	-0.12
2×11	23	0.43***	-0.02	0.10***	-0.11	2.44**
2×12	24**	-0.08	0.03	-0.02	0.02	0.87
2×13	14	0.06	0.14**	-0.01	0.00	0.49
2×14	27	0.41***	0.04	-0.01	-0.05	0.52
2×15	-11	-0.10	0.06*	-0.01	-0.11	0.22
2×16	31	-0.10	-0.00	0.02	-0.13**	-0.33
2×17	10	-0.10	-0.03	-0.07	-0.07	0.60
2×18	15	0.43***	0.02	0.05**	0.26***	-2.85***
2×19	-25**	0.55***	0.01	-0.03	0.08	-0.33
3×6	32*	0.34***	0.01	0.04	0.01	1.67*
3×7	5	-0.31***	0.02	-0.04	0.01	3.20***
3×8	14	-0.06	0.04***	0.02	-0.11	-2.84**
3×9	-4	0.10	-0.12***	0.06	-0.05	-1.31
3×10	-5	0.11	-0.02	0.06**	0.10*	-1.65**
3×11	15	-0.23***	0.07***	0.09**	-0.10	0.61
3×12	12	-0.05	0.05*	0.03	-0.10*	0.21
3×13	12	-0.19**	0.04	-0.01	-0.02	-1.27*
3×14	12	-0.54***	0.02	-0.02	0.03	2.47**
3×15	-7	0.20***	-0.05	0.00	-0.02	0.26
3×16	8	-0.08	0.05*	0.09**	-0.04	-1.36
3×17	12	0.05	-0.08**	-0.05	0.04	1.63
3×18	-11*	0.40***	0.00	0.00	0.03	-2.83***
3×19	11	0.31***	0.06*	-0.02	0.12*	2.51
4×6	11	-0.24*	0.01	0.04*	-0.14**	0.72
4×7	-4	0.04	0.01	-0.01	0.10**	-0.94
4×8	-7	0.09	-0.02	-0.01	-0.14***	1.63*
4×9	28**	0.15*	-0.09***	0.08**	0.00	-1.01
4×10	16	-0.09	0.11***	0.03	-0.02	1.58*
4×11	2	-0.09	0.06*	0.06	-0.17***	1.06
4×12	-28*	-0.17	0.05**	0.01	-0.08	1.23
4×13	-2	-0.29***	0.10**	-0.02	0.01	0.96
4×14	-21	-0.31***	-0.01	-0.04	0.04	-0.07
4×15	6	-0.07	0.05*	0.01	-0.11*	-0.13
4×16	28	-0.01	0.04	0.06**	-0.04	0.70
4×17	-9	0.04	-0.06***	-0.18**	-0.11***	4.39***
4×18	-15*	0.34***	0.03	-0.00	0.28***	0.83
4×19	11	0.55***	0.01	-0.01	-0.01	-1.79*

Continued next page.

Table 2. Continued.

Cross‡	LYLD	Lint%	BW	Mic	E1	T1
5×6	35**	0.27***	−0.06***	0.01	0.12*	−0.55
5×7	15	0.18**	0.03	0.03	0.01	−1.74
5×8	−16	0.07	−0.01	0.01	−0.09	−1.47
5×9	17	0.25***	−0.06**	0.07	0.08	−1.18
5×10	34*	0.21*	0.01	0.04**	0.07	−2.83**
5×11	16	−0.27***	0.03	0.06**	−0.18***	0.40
5×12	11	−0.07	−0.01	−0.03	0.12*	−0.80
5×13	−1	−0.72	0.12**	−0.04*	0.08	−2.25***
5×14	31	0.04	−0.00	−0.04	0.02	−1.07
5×15	27*	−0.03	0.05*	−0.06**	−0.03	−0.58
5×16	32	−0.05	−0.00	0.09***	−0.06	0.02
5×17	0	0.02	−0.05*	−0.10**	0.17**	0.78
5×18	−22	0.11	−0.02	−0.04	0.08	−2.18**
5×19	−2	0.20**	0.08**	−0.07**	0.06	−2.23*

\* Significant at  $P \leq 0.10$ .\*\* Significant at  $P \leq 0.05$ .\*\*\* Significant at  $P \leq 0.01$ .

† Because of rounding small contributions of some traits appears as 0.00 in the table.

‡ Parents for cross are given in Table 1.

ically greater than  $(AA_{ii} + A_{jj})/2$  for most crosses (66 out of 70) for lint yield. Therefore, cotton yield heterosis for these crosses can be fixed at later generation without selection. Additionally, these  $F_2$  populations can be used for pure line selection in early generations. Other crosses showing  $AA_{ij}$  effects greater than zero relative to the mean of  $(AA_{ii} + A_{jj})/2$  included, 14 crosses for lint percentage, 55 for boll weight, 41 for micronaire, 31 for elongation, and 37 for fiber strength. The existence of large  $AA_{ij}$  effects indicate there is a genetic basis for improving yield and fiber quality by fixing heterosis in advanced generations. For example, crosses  $1 \times 15$ ,  $1 \times 19$ ,  $4 \times 9$ ,  $5 \times 6$ , and  $5 \times 10$  could be used to increase yield by exploiting heterosis and/or selecting high yielding lines (Table 2); while crosses  $2 \times 11$ ,  $3 \times 7$ ,  $3 \times 14$ , and  $4 \times 17$  could be used for selecting high strength lines.

### Predicted Hybrid Genotypic Values

The predicted genetic effects were used to calculate hybrid values from  $F_1$  through  $F_6$  for each environment based on the ADAA model for all traits except fiber span length (AD model) under the assumption of no

Table 3. Correlation coefficients between predicted  $F_2$  and  $F_3$  genotypic values and  $F_2$  and  $F_3$  observed values for certain environments.†

Traits	Environment				
	2	3	4	5	6
Lint yield	0.97	0.98	0.98	0.85	0.90
Lint percent	0.96	0.99	0.99	0.98	0.98
Boll weight	0.97	0.98	0.98	0.91	0.85
	Environment				
	1	2	3	4	5
Micronaire	0.57	0.69	0.80	0.69	0.65
Elongation	0.88	0.91	0.78	0.86	0.81
Strength	0.92	0.92	0.94	0.97	0.78
SL50‡	0.68	0.75	0.65	0.66	0.63
SL2.5‡	0.92	0.94	0.93	0.91	0.84

† All estimated values were significant at  $P < 0.01$ . The  $F_2$  agronomic data was from environments 2, 3, and 4 while fiber data was from environments 1, 2, 3, and 4. The  $F_3$  agronomic data was from environments 5 and 6 while fiber data was from environment 5.

‡ 50% and 2.5% span length (SL) were based on AD model.

selection pressure. To detect the efficiency of prediction, we compared the predicted  $F_2$  genotypic values to observed  $F_2$  values for Environments 2, 3, and 4 for agronomic traits, and for Environments 1, 2, 3, and 4 for fiber traits. The predicted  $F_3$  genotypic values were compared to observed  $F_3$  values for Environments 5 and 6 for agronomic traits, and at Environment 5 for fiber traits. The correlation coefficients between observed and predicted values are summarized in Table 3. The results indicated that predicted hybrid values were in good agreement with observed hybrid values for all traits except micronaire reading and 50% span length. Since no additive by additive epistasis effects and small  $AA$  effects were previously detected for 50% span length and 2.5% span length using the ADAA model, it was not appropriate to use this model to predict these two traits, so a reduced model (AD model) was used to provide estimates for these two traits; however, our findings suggest that the use of the ADAA model was appropriate for all other traits.

The results indicate that we may be able to use predicted genotypic values based on statistical analyses to make decisions in our breeding program in early generations. The predicted  $F_6$  genotype values with their mid-

Table 5. Predicted parent values and standard errors across environments for lint yield (LYLD, kg ha<sup>−1</sup>) and fiber strength (T1, kNm kg<sup>−1</sup>).

Parent	LYLD ± SE	T1 ± SE
1. DPL50	838 ± 156	163 ± 9.0
2. DES119	756 ± 139	195 ± 6.5
3. ST474	709 ± 59	189 ± 4.8
4. DPL90	849 ± 112	226 ± 5.6
5. SG125	1027 ± 173	178 ± 6.8
6. M75-1	326 ± 90	241 ± 8.4
7. M1388-1	702 ± 63	239 ± 3.3
8. M1388-2	340 ± 60	282 ± 13.0
9. M1388-3	200 ± 92	279 ± 10.5
10. M239-1	405 ± 134	240 ± 3.0
11. M239-2	271 ± 88	245 ± 5.0
12. M239-3	370 ± 68	268 ± 9.5
13. M239-4	275 ± 86	252 ± 7.3
14. M239-5	299 ± 56	235 ± 4.1
15. M239-6	621 ± 85	250 ± 4.2
16. M239-7	562 ± 111	272 ± 6.8
17. M237-1	305 ± 53	255 ± 5.7
18. M237-2	390 ± 69	247 ± 9.2
19. M237-3	495 ± 120	247 ± 7.8



parent values for lint yield and fiber strength are provided for each cross in Table 4. There was no cross better than the high parent for lint yield (P5) or for fiber strength (P8); however, 66 crosses were numerically greater than mid-parent values for lint yield, 38 crosses were 10% greater than mid-parent values, and 13 crosses were 20% greater than mid-parent values for the lint yield. Most predicted  $F_6$  crosses were significantly greater than their corresponding male parents and were not significantly less than their corresponding female parents (commercial cultivars or better parents) with respect to their predicted lint yield (Tables 4 and 5). On the other hand, most crosses were significantly greater than their corresponding female parents with respect to the predicted fiber strength genotype values. For example, in the predicted  $F_6$  generation, crosses  $5 \times 7$ ,  $5 \times 10$ ,  $5 \times 15$ , and  $5 \times 16$  made high lint yields, which were not significantly less than the female parent 5, while the fiber strength for these crosses was significantly improved compared with their female Parent 5. Similar examples can be also found in Tables 4 and 5. Our study suggested that fiber strength can be significantly improved from their female parents, while lint yields were not significantly less than their female parents for many crosses. This study provided strong evidence that crosses between commercial cultivars and primitive derived lines can produce progeny with improved fiber strength and good yields.

## REFERENCES

- McCarty, J.C., Jr., and J.N. Jenkins. 1993. Registration of 79 day-neutral primitive cotton germplasm lines. *Crop Sci.* 33:351.
- McCarty, J.C., Jr. J. N., Jenkins, and B. Tang. 1995. Primitive cotton germplasm: Variability for yield and fiber traits. *Miss. Agric. and Forestry Exp. Stn. Tech. Bull.* 202.
- McCarty, J.C., Jr., J.N. Jenkins, W.L. Parrott, and R.G. Creech. 1979. The conversion of photoperiodic primitive race stocks of cotton to day-neutral stocks. *Miss. Agric. and Forestry Exp. Res. Rep.* 4(19):4.
- McCarty, J.C., J.N. Jenkins, and J. Wu. 2000. Evaluation of cultivars by race stock F2 hybrids. p. 517–518. *In Proc. Beltwide Cotton Res. Conf.*, San Antonio, TX. 4–8 Jan. 2000. Natl. Cotton Council Am., Memphis, TN.
- McCarty, J.C., J.N. Jenkins, and J. Wu. 2003. Use of primitive accessions of cotton as sources of genes for improving yield components and fiber properties. *Mississippi Agric. and For. Exp. Stn. Bull.* 1130. (Available on-line at <http://msucare.com/pubs/bulletins/b1130.pdf>; verified 5 March 2004).
- McCarty, J.C., J.N. Jenkins, and J. Wu. 2004. Primitive accession derived germplasm by cultivar crosses as sources for cotton improvement: I. Phenotypic values and variance components. *Crop Sci.* 44:1226–1230 (this issue).
- McCarty, J.C., Jr., J.N. Jenkins, and J. Zhu. 1998a. Introgression of day-neutral genes in primitive cotton accessions: I. Genetic variances and correlations. *Crop Sci.* 38:1425–1428.
- McCarty, J.C., Jr., J.N. Jenkins, and J. Zhu. 1998b. Introgression of day-neutral genes in primitive cotton accessions: II. Predicted genetic effects. *Crop Sci.* 38:1428–1431.
- Miller, R.G. 1974. The jackknife-A review. *Biometrika* 61:1–15.
- Percival, A.E. 1987. The national collection of *Gossypium* germplasm. *So. Coop. Series Bull.* 321.
- Van Esbroeck, G., and D.T. Bowman. 1998. Cotton germplasm diversity and its importance to cultivar development. *J. Cotton Sci.* 2:121–129.
- Zhu, J. 1993. Methods of predicting genotype value and heterosis for offspring of hybrids. *J. Biomath.* 8(1):32–44.
- Zhu, J. 1994. General genetic models and new analysis methods for quantitative traits. *J. Zhejiang Agric. Univ.* 20(6):551–559.
- Zhu, J., and B.S. Weir. 1996. Diallel analysis for sex-linked and maternal effects. *Theor. Appl. Genet.* 92:1–9.

**Table 4.** Predicted genotype values for lint yield (LYLD,  $\text{kg ha}^{-1}$ ) and fiber strength (T1,  $\text{kNm kg}^{-1}$ ) at  $F_6$  generation for 70 crosses (5 females by 14 males).

Cross†	MP‡	LYLD $\pm$ SE	$\Delta\%§$	MP	T1 $\pm$ SE	$\Delta\%§$
1×6	582	687 $\pm$ 100	18.0	202	205 $\pm$ 3.9	1.7
1×7	770	771 $\pm$ 76	0.1	201	199 $\pm$ 4.2	-0.9
1×8	589	645 $\pm$ 85	9.6	222	219 $\pm$ 4.2	-1.3
1×9	519	560 $\pm$ 66	7.9	221	214 $\pm$ 2.8	-2.9
1×10	621	673 $\pm$ 74	8.3	201	202 $\pm$ 4.0	0.1
1×11	554	609 $\pm$ 78	9.9	204	207 $\pm$ 4.2	1.5
1×12	604	635 $\pm$ 75	5.1	215	214 $\pm$ 2.7	-0.5
1×13	557	568 $\pm$ 62	2.0	207	201 $\pm$ 2.3	-2.7
1×14	568	645 $\pm$ 107	13.5	199	205 $\pm$ 6.0	2.8
1×15	730	814 $\pm$ 91	11.6	207	210 $\pm$ 5.2	1.8
1×16	700	739 $\pm$ 64	5.6	217	215 $\pm$ 2.4	-1.0
1×17	572	619 $\pm$ 94	8.3	209	213 $\pm$ 6.3	2.0
1×18	614	672 $\pm$ 100	9.5	205	201 $\pm$ 3.2	-2.1
1×19	666	754 $\pm$ 87	13.2	205	200 $\pm$ 3.6	-2.6
2×6	541	691 $\pm$ 88	27.8	218	220 $\pm$ 4.8	0.9
2×7	729	815 $\pm$ 94	11.7	217	220 $\pm$ 3.4	1.3
2×8	548	655 $\pm$ 103	19.6	239	238 $\pm$ 4.8	-0.1
2×9	478	595 $\pm$ 66	24.5	237	238 $\pm$ 5.4	0.4
2×10	580	726 $\pm$ 101	25.2	218	219 $\pm$ 4.0	0.7
2×11	513	653 $\pm$ 105	27.2	220	228 $\pm$ 3.4	3.7
2×12	563	687 $\pm$ 80	22.0	232	234 $\pm$ 2.9	1.1
2×13	516	625 $\pm$ 94	21.1	223	226 $\pm$ 3.1	0.9
2×14	527	664 $\pm$ 129	25.8	215	220 $\pm$ 4.5	2.1
2×15	689	725 $\pm$ 88	5.3	223	225 $\pm$ 4.1	1.0
2×16	659	806 $\pm$ 107	22.3	234	232 $\pm$ 3.3	-0.9
2×17	531	625 $\pm$ 103	17.8	225	229 $\pm$ 3.9	1.6
2×18	573	663 $\pm$ 106	15.7	221	216 $\pm$ 4.9	-2.5
2×19	625	645 $\pm$ 91	3.1	221	222 $\pm$ 2.1	0.2
3×6	517	649 $\pm$ 65	25.5	215	222 $\pm$ 4.1	3.3
3×7	706	748 $\pm$ 37	5.9	214	224 $\pm$ 2.6	4.7
3×8	525	604 $\pm$ 48	15.1	235	229 $\pm$ 6.9	-2.8
3×9	454	513 $\pm$ 44	13.0	234	230 $\pm$ 4.8	-1.7
3×10	557	607 $\pm$ 67	9.1	215	214 $\pm$ 2.4	-0.4
3×11	490	591 $\pm$ 57	20.8	217	222 $\pm$ 2.8	2.2
3×12	539	617 $\pm$ 36	14.4	228	230 $\pm$ 3.7	0.8
3×13	492	572 $\pm$ 49	16.3	220	219 $\pm$ 3.0	-0.4
3×14	504	583 $\pm$ 56	15.7	212	221 $\pm$ 4.7	4.3
3×15	665	687 $\pm$ 56	3.3	220	222 $\pm$ 2.5	1.2
3×16	635	707 $\pm$ 48	11.4	231	227 $\pm$ 5.4	-1.4
3×17	507	584 $\pm$ 63	15.2	222	228 $\pm$ 4.0	2.9
3×18	550	556 $\pm$ 51	1.1	218	213 $\pm$ 4.8	-2.2
3×19	602	678 $\pm$ 43	12.7	218	225 $\pm$ 5.9	3.3
4×6	587	663 $\pm$ 45	12.9	233	237 $\pm$ 6.8	1.4
4×7	776	781 $\pm$ 69	0.7	233	232 $\pm$ 3.4	-0.4
4×8	595	618 $\pm$ 68	4.0	254	254 $\pm$ 9.2	0.2
4×9	525	638 $\pm$ 58	21.7	252	247 $\pm$ 8.3	-2.2
4×10	627	711 $\pm$ 63	13.4	233	236 $\pm$ 3.3	1.5
4×11	560	613 $\pm$ 46	9.6	235	239 $\pm$ 3.8	1.6
4×12	609	588 $\pm$ 66	-3.5	247	249 $\pm$ 6.4	0.8
4×13	562	595 $\pm$ 59	5.8	239	240 $\pm$ 6.1	0.7
4×14	574	572 $\pm$ 64	-0.3	230	232 $\pm$ 2.4	0.8
4×15	735	775 $\pm$ 73	5.4	238	238 $\pm$ 6.1	-0.2
4×16	705	812 $\pm$ 79	15.0	249	248 $\pm$ 6.6	-0.4
4×17	577	597 $\pm$ 54	3.4	240	250 $\pm$ 4.1	4.1
4×18	620	614 $\pm$ 54	-0.9	236	237 $\pm$ 7.0	0.3
4×19	672	735 $\pm$ 75	9.4	236	232 $\pm$ 5.5	-1.7
5×6	676	828 $\pm$ 92	22.5	209	210 $\pm$ 4.2	0.1
5×7	864	929 $\pm$ 81	7.5	209	206 $\pm$ 2.7	-1.3
5×8	683	707 $\pm$ 91	3.4	230	224 $\pm$ 7.1	-2.6
5×9	613	718 $\pm$ 93	17.1	228	222 $\pm$ 4.0	-2.5
5×10	716	853 $\pm$ 114	19.2	209	203 $\pm$ 3.1	-2.9
5×11	649	754 $\pm$ 88	16.3	211	213 $\pm$ 3.8	1.1
5×12	698	785 $\pm$ 85	12.5	223	220 $\pm$ 4.0	-1.2
5×13	651	705 $\pm$ 100	8.4	215	209 $\pm$ 3.0	-2.4
5×14	663	796 $\pm$ 110	20.1	206	206 $\pm$ 4.6	-0.2
5×15	824	920 $\pm$ 112	11.7	214	213 $\pm$ 3.3	-0.6
5×16	794	927 $\pm$ 93	16.7	225	222 $\pm$ 5.7	-1.2
5×17	666	725 $\pm$ 105	8.8	216	218 $\pm$ 4.2	1.0
5×18	708	704 $\pm$ 88	-0.7	212	207 $\pm$ 4.6	-2.7
5×19	761	813 $\pm$ 84	6.9	212	208 $\pm$ 5.8	-2.3

† Parents for cross are given in Table 1.

‡ MP is mid-parent value which is the average genotype value between two parents which are based on combined data over environments.

§  $\Delta\% = (F_6 - MP)/MP \times 100$ .